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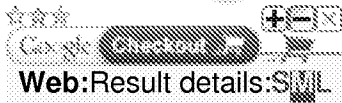


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compare seed article using alignment algorithm


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Scholarly articles for compare seed article using alignment algorithm

-  [BLAT-The BLAST-Like Alignment Tool](#) - Kent - Cited by 1489
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- [Selection of optimal oligonucleotide probes for ...](#) - Li - Cited by 26

1. Using multiple alignments to improve seeded local alignment algorithms

In recent years, the introduction of spaced **seeds** has led to significantly improved local **alignment algorithms** (12,16–20). Spaced **seeds** allow non- contiguous ...
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2. CiteULike: Sequence-specific reconstruction from fragmentary ...

Jul 22, 2008 ... GenSeed is a Perl program that implements a **seed**-driven recursive ...
 10.1093/ bioinformatics/btn283 KW - **algorithm** KW - **alignment** KW ...
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3. Using multiple alignments to improve seeded local alignment ...

Seeds for the BLAST **algorithm** are traditionally fixed-length words present In all tests **using alignment** databases the **alignment** consisted of baboon, ...
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4. 3' UTR seed matches, but not overall identity, are associated with ...

There is an Addendum (June 2006) associated with this **Article**. **Using** the Smith-Waterman **alignment algorithm**, the sense and antisense strands for each ...
www.nature.com/nmeth/journal/v3/n3/full/nmeth854.html - [Similar pages](#)
 by A Birmingham - 2006 - [Cited by 165](#) - [Related articles](#) - [All 5 versions](#)

5. Improved hit criteria for DNA local alignment - Noe, Kucherov ...

0.2: Approximation **Algorithms** For Local **Alignment** With Length. ... 17 Designing **seeds** for similarity search in genomic DNA (context) - BUHLER, KEICH et al. ...
citeseer.ist.psu.edu/633019.html - 25k - [Cached](#) - [Similar pages](#)

6. [BioMed Central | Full text | Automated generation of heuristics ...](#)

Upper bounds dictate that there can be no better **alignment using** these HSPs. This **algorithm** is similar to A* search, (but differs in that many different ...

[www.biomedcentral.com/1471-2105/6/31](#) - 79k - [Cached](#) - [Similar pages](#)
by GSTC Slater - 2005 - [Cited by 89](#) - [Related articles](#) - [All 8 versions](#)

7. [Computer Methods and Programs in Biomedicine : GRAT—genome-scale ...](#)

In a separate step from the **alignment algorithm**, the **seed** database is constructed. Due to memory and time constraints, we could not **compare** the results ...

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by E Kindlund - 2007 - [Cited by 1](#) - [Related articles](#)

8. [Designing **seeds** for similarity search in genomic DNA](#)

Local **alignment** statistics. Methods: a Companion to Methods in Enzymology, 266: 460--80, ... Search **algorithms** for biosequences **using** random projection, 2001 ...

[portal.acm.org/citation.cfm?id=640083](#) - [Similar pages](#)
by J Buhler - 2003 - [Cited by 82](#) - [Related articles](#) - [All 19 versions](#)

9. [IngentaConnect A RAPID **algorithm** for sequence database comparisons ...](#)

These **algorithms** typically use areas of matching words to **seed** alignments ... the word-matching and sequence-**alignment** process, and **using** information about ...

[www.ingentaconnect.com/content/cup/cabios/1999/00000015/00000002/art00111](#)
- [Similar pages](#)
by C Miller - 1999 - [Cited by 29](#) - [Related articles](#) - [All 8 versions](#)

10. [A Clustal **alignment** improver **using** evolutionary **algorithms**](#)

A Clustal **alignment** improver **using** evolutionary **algorithms** ... the wellknown Clustal V **algorithm** as a candidate solution **seed** of the initial EA population. ...

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